


Data processing on the rod-shaped WSSV capsids

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Ring-stacked capsids of white spot syndrome virus and structural transitions with genome ejection

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Detailed protocol

Thanks.

The power spectrum can be calculated via EMAN2 or Relion, which is quite common function in almost all cryo-EM related software.

To obtain the detailed helical parameters for the filaments, you need to index your power spectrum. You can either refer to the tutorial written by MRC group or software packages from Wen Jiang's group in Purdue University.

For WSSV, we did not apply the helical symmetry due to the giant helical rise or multiple helical symmetries, just as what we mentioned in the text. Of course, we did not apply any helical symmetry during our 2D or 3D classifications.

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Zhang, Y. and Shen, Q. (2023). Data processing on the rod-shaped WSSV capsids. Bio-protocol Preprint. bio-protocol.org/prep2179.
2. Sun, M., Liu, M., Shan, H., Li, K., Wang, P., Guo, H., Zhao, Y., Wang, R., Tao, Y., Yang, L., Zhang, Y., Su, X., Liu, Y., Li, C., Lin, J., Chen, X., Zhang, Y. and Shen, Q. (2023). Ring-stacked capsids of white spot syndrome virus and structural transitions with genome ejection. Science Advances 9(8). DOI: [10.1126/sciadv.add2796](https://doi.org/10.1126/sciadv.add2796)

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